

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/522,074
Source: 25/10
Date Processed by STIC: 8/22/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER** **VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>>., EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

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Raw Sequence Listing Error Summary

SUGGESTED CORRECTION

SERIAL NUMBER: 10/522,074

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | |
|----|---|
| 1 | <div style="border: 1px solid black; padding: 5px;"> <div style="display: flex; justify-content: space-between;"> <div style="width: 20%;"> <p>____ Wrapped Nucleics
 Wrapped Aminos</p> </div> <div style="width: 80%;"> <p>The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."</p> </div> </div> </div> |
| 2 | <div style="border: 1px solid black; padding: 5px;"> <div style="display: flex; justify-content: space-between;"> <div style="width: 20%;"> <p>____ Invalid Line Length</p> </div> <div style="width: 80%;"> <p>The rules require that a line not exceed 72 characters in length. This includes white spaces.</p> </div> </div> </div> |
| 3 | <div style="border: 1px solid black; padding: 5px;"> <div style="display: flex; justify-content: space-between;"> <div style="width: 20%;"> <p>____ Misaligned Amino
 Numbering</p> </div> <div style="width: 80%;"> <p>The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers: use space characters, instead.</p> </div> </div> </div> |
| 4 | <div style="border: 1px solid black; padding: 5px;"> <div style="display: flex; justify-content: space-between;"> <div style="width: 20%;"> <p>____ Non-ASCII</p> </div> <div style="width: 80%;"> <p>The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.</p> </div> </div> </div> |
| 5 | <div style="border: 1px solid black; padding: 5px;"> <div style="display: flex; justify-content: space-between;"> <div style="width: 20%;"> <p>____ Variable Length</p> </div> <div style="width: 80%;"> <p>Sequence(s)____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.</p> </div> </div> </div> |
| 6 | <div style="border: 1px solid black; padding: 5px;"> <div style="display: flex; justify-content: space-between;"> <div style="width: 20%;"> <p>____ PatentIn 2.0
 "bug"</p> </div> <div style="width: 80%;"> <p>A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.</p> </div> </div> </div> |
| 7 | <div style="border: 1px solid black; padding: 5px;"> <div style="display: flex; justify-content: space-between;"> <div style="width: 20%;"> <p>____ Skipped Sequences:
 (OLD RULES)</p> </div> <div style="width: 80%;"> <p>Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped</p> <p>Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.</p> </div> </div> </div> |
| 8 | <div style="border: 1px solid black; padding: 5px;"> <div style="display: flex; justify-content: space-between;"> <div style="width: 20%;"> <p>____ Skipped Sequences
 (NEW RULES)</p> </div> <div style="width: 80%;"> <p>Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000</p> </div> </div> </div> |
| 9 | <div style="border: 1px solid black; padding: 5px;"> <div style="display: flex; justify-content: space-between;"> <div style="width: 20%;"> <p>____ Use of n's or Xaa's
 (NEW RULES)</p> </div> <div style="width: 80%;"> <p>Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.</p> </div> </div> </div> |
| 10 | <div style="border: 1px solid black; padding: 5px;"> <div style="display: flex; justify-content: space-between;"> <div style="width: 20%;"> <p>____ Invalid <213>
 Response</p> </div> <div style="width: 80%;"> <p>Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence</p> </div> </div> </div> |
| 11 | <div style="border: 1px solid black; padding: 5px;"> <div style="display: flex; justify-content: space-between;"> <div style="width: 20%;"> <p>____ Use of <220></p> </div> <div style="width: 80%;"> <p>Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)</p> </div> </div> </div> |
| 12 | <div style="border: 1px solid black; padding: 5px;"> <div style="display: flex; justify-content: space-between;"> <div style="width: 20%;"> <p>____ PatentIn 2.0
 "bug"</p> </div> <div style="width: 80%;"> <p>Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.</p> </div> </div> </div> |
| 13 | <div style="border: 1px solid black; padding: 5px;"> <div style="display: flex; justify-content: space-between;"> <div style="width: 20%;"> <p>____ Misuse of n/Xaa</p> </div> <div style="width: 80%;"> <p>"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid</p> </div> </div> </div> |

AMC – Biotechnology Systems Branch – 09/09/2003

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PCT

RAW SEQUENCE LISTING

DATE: 08/22/2005

PATENT APPLICATION: US/10/522,074

TIME: 17:07:34

Input Set : A:\10-522,074 SEQLIST 20050630.txt

Output Set: N:\CRF4\08222005\J522074.raw

3 <110> APPLICANT: Delta Biotechnology Limited
 4 Darrell Sleep
 6 <120> TITLE OF INVENTION: Gene and Polypeptide Sequences
 8 <130> FILE REFERENCE: P30,358 USA
 10 <140> CURRENT APPLICATION NUMBER: 10/522,074
 C--> 11 <141> CURRENT FILING DATE: 2005-01-21
 13 <150> PRIOR APPLICATION NUMBER: PCT/GB2003/003273
 14 <151> PRIOR FILING DATE: 2003-07-23
 16 <150> PRIOR APPLICATION NUMBER: GB 0217033.0
 17 <151> PRIOR FILING DATE: 2002-07-23
 19 <160> NUMBER OF SEQ ID NOS: 40
 21 <170> SOFTWARE: SeqWin99
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 5
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Artificial Sequence
 28 <220> FEATURE:
 29 <223> OTHER INFORMATION: Leader sequence
 31 <220> FEATURE:
 32 <221> NAME/KEY: MISC_FEATURE
 33 <222> LOCATION: 1
 34 <223> OTHER INFORMATION: CAN BE EITHER Phe OR Trp OR Tyr
 36 <220> FEATURE:
 37 <221> NAME/KEY: MISC_FEATURE
 38 <222> LOCATION: 2
 39 <223> OTHER INFORMATION: CAN BE EITHER Ile OR Leu OR Val OR Ala OR Met
 41 <220> FEATURE:
 42 <221> NAME/KEY: MISC_FEATURE
 43 <222> LOCATION: 3
 44 <223> OTHER INFORMATION: CAN BE EITHER Leu OR Val OR Ala OR Met
 46 <220> FEATURE:
 47 <221> NAME/KEY: MISC_FEATURE
 48 <222> LOCATION: 4
 49 <223> OTHER INFORMATION: CAN BE EITHER Ser OR Thr
 51 <220> FEATURE:
 52 <221> NAME/KEY: MISC_FEATURE
 53 <222> LOCATION: 5
 54 <223> OTHER INFORMATION: CAN BE EITHER Ile OR Val OR Ala OR Met
 56 <400> SEQUENCE: 1
 57 Phe Ile Leu Ser Ile
 58 1 5
 60 <210> SEQ ID NO: 2
 61 <211> LENGTH: 5

pr 1-b
 Does Not Comply
 corrected Diskette Needed

What is the source of genetic material?
 "Phe can only represent itself."
 Use "Xaa" instead (see item 11 on Euro summary sheet)
 And explain in 2207-2237 section
 same error

RAW SEQUENCE LISTING

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Input Set : A:\10-522,074 SEQLIST 20050630.txt

Output Set: N:\CRF4\08222005\J522074.raw

62 <212> TYPE: PRT
 63 <213> ORGANISM: Artificial Sequence
 65 <220> FEATURE:
 66 <223> OTHER INFORMATION: Leader sequence
 68 <220> FEATURE:
 69 <221> NAME/KEY: MISC_FEATURE
 70 <222> LOCATION: 2
 71 <223> OTHER INFORMATION: CAN BE EITHER Ile OR Leu OR Val OR Ala OR Met
 73 <220> FEATURE:
 74 <221> NAME/KEY: MISC_FEATURE
 75 <222> LOCATION: 3
 76 <223> OTHER INFORMATION: CAN BE EITHER Leu OR Val OR Ala OR Met
 78 <220> FEATURE:
 79 <221> NAME/KEY: MISC_FEATURE
 80 <222> LOCATION: 4
 81 <223> OTHER INFORMATION: CAN BE EITHER Ser OR Thr
 83 <220> FEATURE:
 84 <221> NAME/KEY: MISC_FEATURE
 85 <222> LOCATION: 5
 86 <223> OTHER INFORMATION: CAN BE EITHER Ile OR Val OR Ala OR Met
 88 <400> SEQUENCE: 2
 89 Phe Ile Leu Ser Ile
 90 1 5
 92 <210> SEQ ID NO: 3
 93 <211> LENGTH: 5
 94 <212> TYPE: PRT
 95 <213> ORGANISM: Artificial Sequence
 97 <220> FEATURE:
 98 <223> OTHER INFORMATION: Leader sequence
 100 <220> FEATURE:
 101 <221> NAME/KEY: MISC_FEATURE
 102 <222> LOCATION: 1
 103 <223> OTHER INFORMATION: CAN BE EITHER Phe OR Trp OR Tyr
 105 <220> FEATURE:
 106 <221> NAME/KEY: MISC_FEATURE
 107 <222> LOCATION: 3
 108 <223> OTHER INFORMATION: CAN BE EITHER Leu OR Val OR Ala OR Met
 110 <220> FEATURE:
 111 <221> NAME/KEY: MISC_FEATURE
 112 <222> LOCATION: 4
 113 <223> OTHER INFORMATION: CAN BE EITHER Ser OR Thr
 115 <220> FEATURE:
 116 <221> NAME/KEY: MISC_FEATURE
 117 <222> LOCATION: 5
 118 <223> OTHER INFORMATION: CAN BE EITHER Ile OR Val OR Ala OR Met
 120 <400> SEQUENCE: 3
 121 Phe Ile Leu Ser Ile
 122 1 5
 124 <210> SEQ ID NO: 4

same error
use Xaa and explain

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/522,074

DATE: 08/22/2005

TIME: 17:07:34

Input Set : A:\10-522,074 SEQLIST 20050630.txt

Output Set: N:\CRF4\08222005\J522074.raw

125 <211> LENGTH: 5
 126 <212> TYPE: PRT
 127 <213> ORGANISM: Artificial Sequence
 129 <220> FEATURE:
 130 <223> OTHER INFORMATION: Leader sequence
 132 <220> FEATURE:
 133 <221> NAME/KEY: MISC_FEATURE
 134 <222> LOCATION: 1
 135 <223> OTHER INFORMATION: CAN BE EITHER Phe OR Trp OR Tyr
 137 <220> FEATURE:
 138 <221> NAME/KEY: MISC_FEATURE
 139 <222> LOCATION: 2
 140 <223> OTHER INFORMATION: CAN BE EITHER Ile OR Leu OR Val OR Ala OR Met
 142 <220> FEATURE:
 143 <221> NAME/KEY: MISC_FEATURE
 144 <222> LOCATION: 4
 145 <223> OTHER INFORMATION: CAN BE EITHER Ser OR Thr
 147 <220> FEATURE:
 148 <221> NAME/KEY: MISC_FEATURE
 149 <222> LOCATION: 5
 150 <223> OTHER INFORMATION: CAN BE EITHER Ile OR Val OR Ala OR Met
 152 <400> SEQUENCE: 4
 153 Phe Ile Val Ser Ile
 154 1 5
 156 <210> SEQ ID NO: 5
 157 <211> LENGTH: 5
 158 <212> TYPE: PRT
 159 <213> ORGANISM: Artificial Sequence
 161 <220> FEATURE:
 162 <223> OTHER INFORMATION: Leader sequence
 164 <220> FEATURE:
 165 <221> NAME/KEY: MISC_FEATURE
 166 <222> LOCATION: 1
 167 <223> OTHER INFORMATION: CAN BE EITHER Phe OR Trp OR Tyr
 169 <220> FEATURE:
 170 <221> NAME/KEY: MISC_FEATURE
 171 <222> LOCATION: 2
 172 <223> OTHER INFORMATION: CAN BE EITHER Ile OR Leu OR Val OR Ala OR Met
 174 <220> FEATURE:
 175 <221> NAME/KEY: MISC_FEATURE
 176 <222> LOCATION: 3
 177 <223> OTHER INFORMATION: CAN BE EITHER Leu OR Val OR Ala OR Met
 179 <220> FEATURE:
 180 <221> NAME/KEY: MISC_FEATURE
 181 <222> LOCATION: 5
 182 <223> OTHER INFORMATION: CAN BE EITHER Ile Val OR Ala OR Met
 184 <400> SEQUENCE: 5
 185 Phe Ile Leu Ser Ile
 186 1 5

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/522,074

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TIME: 17:07:34

Input Set : A:\10-522,074 SEQLIST 20050630.txt

Output Set: N:\CRF4\08222005\J522074.raw

188 <210> SEQ ID NO: 6
189 <211> LENGTH: 5
190 <212> TYPE: PRT
191 <213> ORGANISM: Artificial Sequence
193 <220> FEATURE:
194 <223> OTHER INFORMATION: Leader sequence
196 <220> FEATURE:
197 <221> NAME/KEY: MISC_FEATURE
198 <222> LOCATION: 1
199 <223> OTHER INFORMATION: CAN BE EITHER Phe OR Trp OR Tyr
201 <220> FEATURE:
202 <221> NAME/KEY: MISC_FEATURE
203 <222> LOCATION: 2
204 <223> OTHER INFORMATION: CAN BE EITHER Ile OR Leu OR Val OR Ala OR Met
206 <220> FEATURE:
207 <221> NAME/KEY: MISC_FEATURE
208 <222> LOCATION: 3
209 <223> OTHER INFORMATION: CAN BE EITHER Leu OR Val OR Ala OR Met
211 <220> FEATURE:
212 <221> NAME/KEY: MISC_FEATURE
213 <222> LOCATION: 4
214 <223> OTHER INFORMATION: CAN BE EITHER Ser OR Thr
216 <400> SEQUENCE: 6
217 Phe Ile Leu Ser Ile
218 1 5
220 <210> SEQ ID NO: 7
221 <211> LENGTH: 5
222 <212> TYPE: PRT
223 <213> ORGANISM: Artificial Sequence
225 <220> FEATURE:
226 <223> OTHER INFORMATION: Leader sequence
228 <400> SEQUENCE: 7
229 Phe Ile Val Ser Ile
230 1 5
232 <210> SEQ ID NO: 8
233 <211> LENGTH: 4
234 <212> TYPE: PRT
235 <213> ORGANISM: Artificial Sequence
237 <220> FEATURE:
238 <223> OTHER INFORMATION: Leader sequence
240 <400> SEQUENCE: 8
241 Met Lys Trp Val
242 1
244 <210> SEQ ID NO: 9
245 <211> LENGTH: 9
246 <212> TYPE: PRT
247 <213> ORGANISM: Artificial Sequence
249 <220> FEATURE:
250 <223> OTHER INFORMATION: Leader sequence

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/522,074

DATE: 08/22/2005

TIME: 17:07:34

Input Set : A:\10-522,074 SEQLIST 20050630.txt

Output Set: N:\CRF4\08222005\J522074.raw

global error
 The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

252 <400> SEQUENCE: 9
 253 Leu Phe Leu Phe Ser Ser Ala Tyr Ser
 254 1 5
 256 <210> SEQ ID NO: 10
 257 <211> LENGTH: 9
 258 <212> TYPE: PRT
 259 <213> ORGANISM: Artificial Sequence
 261 <220> FEATURE:
 262 <223> OTHER INFORMATION: Leader sequence
 264 <220> FEATURE:
 265 <221> NAME/KEY: MISC_FEATURE
 266 <222> LOCATION: 1
 267 <223> OTHER INFORMATION: CAN BE EITHER Ile OR Leu OR Val OR Ala OR Met
 269 <220> FEATURE:
 270 <221> NAME/KEY: MISC_FEATURE
 271 <222> LOCATION: 2
 272 <223> OTHER INFORMATION: CAN BE EITHER Phe OR Trp OR Tyr
 274 <220> FEATURE:
 275 <221> NAME/KEY: MISC_FEATURE
 276 <222> LOCATION: 3
 277 <223> OTHER INFORMATION: CAN BE EITHER Ile OR Leu OR Val OR Ala OR Met
 279 <220> FEATURE:
 280 <221> NAME/KEY: MISC_FEATURE
 281 <222> LOCATION: 4
 282 <223> OTHER INFORMATION: CAN BE EITHER Phe OR Trp OR Tyr
 284 <220> FEATURE:
 285 <221> NAME/KEY: MISC_FEATURE
 286 <222> LOCATION: 5
 287 <223> OTHER INFORMATION: CAN BE EITHER Ser OR Thr OR Gly OR Tyr OR Ala
 289 <220> FEATURE:
 290 <221> NAME/KEY: MISC_FEATURE
 291 <222> LOCATION: 6
 292 <223> OTHER INFORMATION: CAN BE EITHER Ser OR Thr OR Gly OR Tyr OR Ala
 294 <220> FEATURE:
 295 <221> NAME/KEY: MISC_FEATURE
 296 <222> LOCATION: 7
 297 <223> OTHER INFORMATION: CAN BE EITHER Ile OR Leu OR Val OR Ala OR Met
 299 <220> FEATURE:
 300 <221> NAME/KEY: MISC_FEATURE
 301 <222> LOCATION: 8
 302 <223> OTHER INFORMATION: CAN BE EITHER Phe OR Trp OR Tyr
 304 <220> FEATURE:
 305 <221> NAME/KEY: MISC_FEATURE
 306 <222> LOCATION: 9
 307 <223> OTHER INFORMATION: CAN BE EITHER Ser OR Thr OR Gly OR Tyr OR Ala
 309 <400> SEQUENCE: 10
 310 Ile Phe Ile Phe Ser Ser Ile Phe Ser
 311 1 5
 313 <210> SEQ ID NO: 11

RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : A:\10-522,074 SEQLIST 20050630.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:12; Xaa Pos. 5,6,7,8,9
Seq#:13; Xaa Pos. 5,6,7,8,9
Seq#:14; Xaa Pos. 5,6,7,8,9
Seq#:15; N Pos. 12
Seq#:16; N Pos. 9,12
Seq#:31; Xaa Pos. 5,6,7,8,9

VERIFICATION SUMMARY

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Input Set : A:\10-522,074 SEQLIST 20050630.txt

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:359 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:399 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
L:439 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:480 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:496 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:915 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0